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Disease Update from the Global Amphibian and Reptile Disease Conference and the World Congress of Herpetology, Kuching, Malaysia, August 2024

Herpetofaunal diseases were a dominant theme in meeting rooms at the Borneo Convention Center in Kuching, Malaysia, where the 2024 Global Amphibian and Reptile Disease Conference (GARD24: Fig. 1) convened with the 10th World Congress of Herpetology (WCH10), 5–9 August 2024. Disease topics were addressed in 133 abstracts, representing 9% of all joint-meeting submissions (available online; Das 2024), covering work on 15 categories of disease agents across 34 nations. Although diseases are natural components of ecosystems, this relatively large proportion of amphibian and reptile disease papers reflects recent advances in understanding the distribution and impact of pathogens and parasites, along with rising concern for emerging herpetofaunal diseases affecting novel species and geographies that are contributing to population declines (Langwig et al. 2015; Luedtke et al. 2023; Bletz et al. 2024).

Preplanning to gauge interest in disease presentations at this joint meeting aided coordination of sessions and ensured a broad representation of speakers and topics. GARD24 travel grants facilitated attendance by 25 students and early-career professionals from 21 countries (Healthy Amphibian Trade Team 2024), adding diverse perspectives and content to three days of GARD24 oral sessions. To allow access to presentations, GARD24 talks were recorded by delegates from the University of Tennessee, Knoxville, USA (available online; Healthy Amphibian Trade Team 2024). Additional disease presentations were scheduled in oral and poster sessions of the WCH10, where talks on diverse herpetological topics convened concurrently across 14 meeting rooms. Adjoining hallways offered poster viewing and networking opportunities for ca. 1500 conference delegates.

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Herein, we provide examples that illustrate the breadth and depth of presentations on herpetofaunal disease agents (including micro- and macro-parasites) and discuss challenges and next steps for international herpetofaunal disease research. Our summary omits presentations on general topics of microbiome communities, immunology, and toxicology where infectious pathogens as disease agents were not specified in the abstracts. Although the World Health Organization has categorized snakebite envenoming as a disease (WHO 2019), we did not include this topic in our synthesis.

REPTILE DISEASE HIGHLIGHTS

Reptiles were the focus of approximately 27% of disease abstracts (N = 36 of 133 abstracts; including 8 presentations that also covered amphibian work), considerably more than the 16% of reptile-pathogen presentations at the first GARD conference in 2022 in Knoxville, Tennessee, USA (GARD22: Gray et al. 2023a; see also Olson et al. 2022; GARD22 program with abstracts available at https://utconferences.eventsair.com/gard-conference/, accessed 10 Sept 2024). Gray et al. (2023a) previously speculated that the smaller number of reptile presentations, compared to those addressing amphibian pathogens, might reflect funding biases.

At the GARD24 and WCH10 sessions, 12 turtle presentations addressed key disease agents including *Ranavirus* (*Rv*), *Fusarium*, and *Cryptosporidium*, and ectoparasites such as ticks. For example, Amarga et al. (2024) examined the taxonomy, geographic history, and host species of the Asian Turtle Tick *Amblyomma geoemydae*; their results supported the identification of an undescribed new species, underscoring the need for additional phylogenetic analyses of reptile ectoparasites. Kuschke et al. (2024) examined the potential presence and threats of fungal infection by members of the *Fusarium solani* species complex (which includes over 45 identifiable species) in Leatherback Sea Turtle (*Dermochelys coriacea*) hatchlings in Florida, USA, and Carranco et al. (2024) explored the role of symbiotic turtle egg microbiota in *Fusarium* fungal infection resistance in Yellow-Spotted Amazon River Turtles (*Podocnemis unifilis*). Additionally, Gielens and Walton (2024) reported that treatment with Ponazuril and Humatin reduced mortality from infection with the protozoan parasite *Cryptosporidium* from 36% to 2% in Western Painted Turtle (*Chrysemys picta bellii*) hatchlings in Canada. Relatedly, Simpson (2024) discussed the importance of screening for *Cryptosporidium* in captive and released pet turtles in the United Kingdom.

Eleven presentations on lizards highlighted diseases caused by *Rv*, ectoparasites, endoparasites, and hemoparasites. Harman et al. (2024) addressed the concept of invasive species spillover and spillback in their study from the southeastern United States, where invasive Argentine Giant Tegus (*Salvator merianae*)

PHOTO BY MATTHEW GRAY

FIG. 1. Participants in the Global Amphibian and Reptile Disease 2024 Conference at the August 2024 World Congress of Herpetology 10, Kuching, Malaysia.

from South America serve as definitive hosts for invasive snake lungworms (*Raillietiella orientalis*) from Southeast Asia. Additionally, Terry and Foufopoulos (2024) reported sex-specific responses to infection with the hemoparasite *Hepatazoon* in Erhard's Wall Lizards (*Podarcis erhardii*) in Greece, and Picelli et al. (2024) used molecular and microscopic techniques to comprehensively assess hidden hemoparasite diversity in lizards, snakes, chelonians, and anurans in Namibia and Angola.

Seven snake presentations covered a range of topics including viruses, hemoparasites, and snake fungal disease. A poster by Cook et al. (2024) reported a dearth of knowledge about parasites infecting their 168 snake species in South Africa. They screened 154 snakes from five genera and seven species for blood parasites, specifically hemoprotozoa of the genus *Hepatozoon*. They found that 49 (ca. 32%) snakes were infected with possibly three parasite species. Snake species with a more diverse diet appeared to harbor a greater diversity of *Hepatozoon* species. Joudrier et al. (2024) reported a 28% prevalence of snake fungal disease in their surveillance from Switzerland, supporting the presence of both European and North American lineages of *Ophidiomyces ophidiicola* (*Oo*) and showing an association between *Oo* occurrence and human disturbance. Despite these insights, they emphasized the need for further research on how diseases affect snake physiology and behavior at sublethal levels, which is essential for understanding the full impacts on snake populations. Haydt et al. (2024) modeled ophidiomycosis occurrence in the USA and incorporated available soil microbiota, soil moisture, and land-use data. They found that soil moisture and human modification both affected soil microbiota, and human modification had the largest impact on the predicted probability of ophidiomycosis occurrence. Two bacterial genera and two fungal genera in soils accounted for the highest amount of variability in ophidiomycosis occurrence. These preliminary findings demonstrate the importance of understanding the interactions of anthropogenic factors such as land use with the community ecology of soil and ophidiomycosis.

AMPHIBIAN DISEASE HIGHLIGHTS

Amphibians dominated presentations with 104 of 133 (78%) disease abstracts addressing all three Orders: Anura (N = 71), Caudata (N = 19), and Gymnophiona (N = 3). Given the decades-long history of global amphibian population declines and species extinctions which led to the description of chytridiomycosis caused by *Batrachochytrium dendrobatidis* (*Bd*: Longcore et al. 1999) and its congener *B. salamandrivorans* (*Bsal*: Martel et al. 2013; see related papers: O'Hanlon et al. 2018; Scheele et al. 2019; Fisher and Garner 2020; Lötters et al. 2020; Luedtke et al. 2023), it is unsurprising that these two fungal pathogens were the focus of more than half of the disease presentations (79 of 133, 59%). *Bd* was the dominant disease agent represented (72 abstracts [54% of all abstracts]; Fig. 2), across 5 of 6 world geographies (Fig. 3). *Bsal* was represented in 18 abstracts, making it the third most-frequent pathogen group (Fig. 2); some of these abstracts also addressed other pathogens such as *Bd* and *Rv*. Chytrid presentations similarly dominated the previous GARD22 conference, where it was discussed in 56% of presentations (Gray et al. 2023a).

Bd presentations spanned new reports of historical or contemporary occurrences, genetic variants, the effects on individuals of *Bd* infection (behavior, movements, body

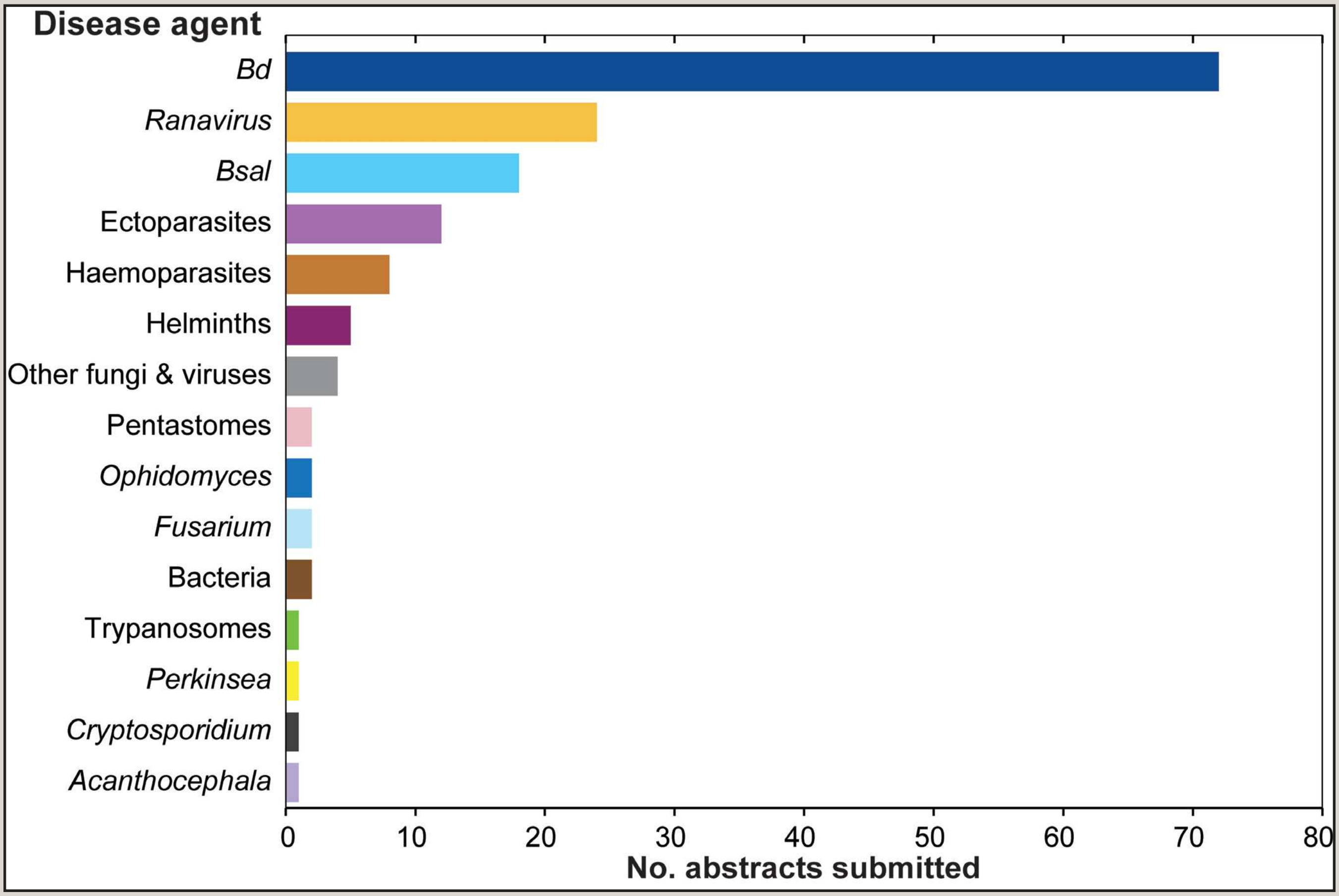

Fig. 2. Frequency of 15 categories of main disease agents in 133 abstracts submitted to the joint sessions of the Global Amphibian and Reptile Disease 2024 Conference and the World Congress of Herpetology 10, Kuching, Malaysia. Some abstracts included studies of multiple disease agents; each occurrence was counted. *Bd* = *Batrachochytrium dendrobatidis*; *Bsal* = *B. salamandrivorans* (amphibian chytrid fungi).

condition, survival), and climate interactions. Karthikeyan Vasudevan's GARD24 Keynote talk (Vasudevan 2024) reported the challenge of diagnostic uncertainties for *Bd* surveillance in India, a nation where *Bd* infections result in no disease signs in hosts in correspondence to *Bd* having a long evolutionary history on the continent with endemic amphibians. He also spoke about local *Bd* variants exhibiting gene-sequence insertion, deletion, and substitution of bases, which can result in false-negative laboratory results using standard diagnostic techniques. Ben Scheele's GARD24 Keynote talk (Scheele 2024) addressed how *Bd* has been a selective force in hosts susceptible to *Bd* chytridiomycosis in Australia, changing the ecology of species, driving niche contractions (Scheele et al. 2023), and how *Bd* may influence life-history traits such as early maturation, resulting in elevated importance for some species' persistence as old age increased vulnerabilities to recruitment failures (Heard et al. 2024; Scheele et al. 2024).

In a WCH10 symposium on the Amphibian Biology Series of publications in the Great Hall of the Borneo Convention Center, Lee Berger and colleagues from Australia provided an overview of amphibian fungal diseases (Berger et al. 2024). They included a range of interim mitigation measures (e.g., captive breeding, antifungal applications) designed to "*buy time*" and stop extinctions while research trials seek long-term solutions (e.g., management of disease-free wildlife reserves, increasing host resistance, translocation of resistant populations, microbiome and genetic solutions to enhance disease resistance).

In a GARD24 Keynote talk, Richard Griffiths (Griffiths 2024) of the United Kingdom discussed how "the rise of emerging infectious diseases (EIDs) fundamentally changed approaches to amphibian conservation." For example, EIDs have influenced the One Plan Approach for Conservation (e.g., Byers et al. 2013; Gray et al. 2023a), in which multiple stakeholders develop combined *in situ* and *ex situ* conservation solutions. Previously, such collaborations between science, management, and wild versus captive sectors of amphibian conservation programs were not well developed. Griffiths also acknowledged how disease outbreaks changed the direction of zoos in the 2000s (just after *Bd* was described; Longcore et al. 1999). Zoos transitioned into becoming arks to sustain perceived doomed species of broader taxonomic groups including amphibians, adding a new captive dimension to risk-management strategies, again with the notion of "*buying them time*" until reintroductions were hoped to become feasible as multiple threat factors could be reconciled. Presentations by Drs. Scheele, Berger, and Griffiths conveyed both a hopeful future beyond *Bd,* where natural processes might allow for host-pathogen coexistence, or a form of managed coexistence could be developed to balance the tide of species' losses.

Bsal is causing disease-related population declines in European salamanders (e.g., Martel et al. 2013, 2014; Lötters et al. 2020), and if/when introduced there is projected to cause similar issues for North American species where it has not yet been detected (Waddle et al. 2020; Gray et al. 2023b; Olson et

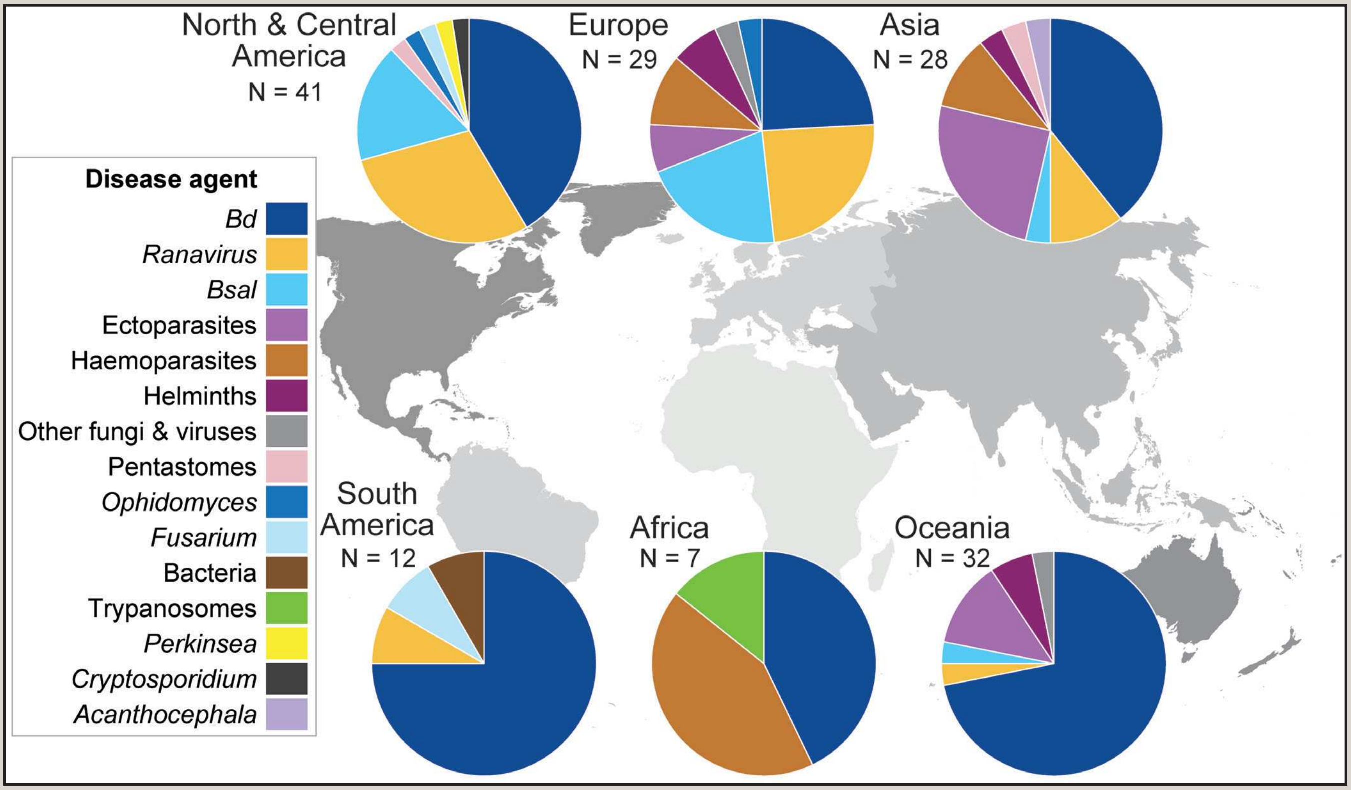

Fig. 3. Geographic distribution of 15 categories of disease agents in studies from 133 abstracts submitted to the joint sessions of the Global Amphibian and Reptile Disease 2024 Conference and the World Congress of Herpetology 10, Kuching, Malaysia. N = no. disease agents named in studies by geographic area; some abstracts addressed multiple disease agents.

al. 2024). Matt Gray summarized *Bsal* research findings from North America in a WCH10 Plenary talk (Gray 2024). More than 140 North American species are likely to be susceptible to *Bsal* chytridiomycosis and could experience population declines if exposed to this novel infectious agent. Models suggest the current risk of *Bsal* invasion is highest in the US Northwest, with pockets of the US West landscape having high extinction risk owing to the presence of many *Bsal*-susceptible taxa. However, the greatest biodiversity loss from *Bsal* disease is expected to occur in the Appalachian region of the eastern USA. The greatest diversity of *Bsal*-resistant species is modeled for the Upper Midwest, USA. Gray's *Bsal* update from North American studies included recent advances in climate-niche modeling and climate change effects reported for *Bsal*-susceptible caudates in the USA by Grisnik et al. (2023), as well as the projected elevated role of the Eastern Newt (*Notophthalmus viridescens*) in the epidemiology of *Bsal* transmission (Malagon et al. 2020; Tompros et al. 2021; Carter et al. 2024).

The joint meeting also featured additional reports on a variety of amphibian disease agents and their synergies with interacting factors. For example, Rachel Marschang spoke about concerns for amphibians in northern Germany (Marschang et al. 2024), where surveillance did not detect *Rv* or *Bsal* infections, but identified two types of herpesvirus—ranid herpesvirus 3 (RaHV3) and bufonid herpesvirus 1 (BfHV1)—alongside *Bd*. She suggested that population declines in her study area might be driven by multiple factors and called for further research into the interactions of disease agents. Olvera Avila and Parra Olea (2024) reported low *Rv* and high *Bd* presence in high-elevation temperate areas from Central Mexico, where land use and *Bd* chytridiomycosis may be contributing to population declines. Lastly, Retuci Pontes and colleagues (Retuci Pontes et al. 2024) examined the potential role of climate fluctuations in *Bd* infections in the microendemic and critically endangered toad *Melanophryniscus admirabilis* in Brazil. Their results suggested climate anomalies (temperatures exceeding normal averages) were associated with *Bd* transmission and infection status. Despite over two decades of focused *Bd* research (e.g., Blaustein et al. 2018; Fisher and Garner 2020), these reports from several continents demonstrate that we are still on the learning curve of the intricate dynamics of *Bd*-host ecological interactions.

Future Directions

The disease papers at this conference support the growing disciplines of herpetofaunal disease ecology and epidemiology, with 15 categories of disease agents dominating investigations (Fig. 2). The advances highlighted above reflect the state of disease science across geographies (Fig 3) and can inform the next steps in disease science and management. In this light, amphibian and reptile disease studies reporting parasite or pathogen *occurrence* or *prevalence* patterns among host species and geographies often dominated presentations. Although this is important information that can lead to more specific focal research to gain understanding of the effects of infection behaviorally, physiologically, epidemiologically, ecologically, and at scales of biological organization larger than individual hosts such as populations and communities, it appears to represent the nascent stages of scientific research for most diseases. An understanding of severe threats to local fauna is a conservation objective for host-species sustainability, but a broader conceptual basis of the ramifications of the disease-agent occurrence can appear lacking. The relative maturity and complexity of the topics addressed by some of the *Bd* presentations seemed to integrate ecological or epidemiological theory, more tangible long-term effects of *Bd* impacts, and conservation or resolution pathways being studied. Acceleration of the pace of work beyond disease agent occurrences toward studies addressing hypothesis testing in physiological or ecological domains and for actionable mitigations is hoped to draw focused attention in coming years.

We noted an evident pattern of higher numbers of disease studies in north-temperate zones and Australia (Fig. 3). This could be a societal bias of meeting attendees, a representation of greater socioeconomic resources toward a broader suite of emerging infections of concern in these geographies, and/or a true pattern of higher disease threat in some geographies. For example, that last option may be garnering support with the recognition that both *Bd* and *Bsal* appear to have evolutionary origins in Asia and relatively recent transmission to other continents (e.g., Martel et al. 2014; Laking et al. 2017; O'Hanlon et al. 2018). Also, there is supporting evidence that variants of *Ophidiomyces ophidiicola* (fungal pathogen causing snake fungal disease) may have been transmitted to Europe and North America relatively recently (Franklinos et al. 2017; Ladner et al. 2022). Pathogens as invasive species are part of the ecological process of ongoing biotic homogenization globally. More generally, the threat of invasive species is ranked notably higher for amphibians in the Nearctic realm of North America than other world regions, ranking third among threats in that geography after habitat loss and climate change, which was higher than for all other regions assessed by the recent Global Amphibian Assessment 2 (GAA2: see Re:wild, Synchronicity Earth, IUCN SSC Amphibian Specialist Group 2023; Luedtke et al. 2023). This pattern seems to track migratory patterns of humans and associated intentional and unintentional movement of biota and fomites in the last few hundred years. An integrated risk of two threat factors, invasive species and disease, merits closer attention informed by research that integrates microbial ecology, vertebrate ecology, and epidemiology. For example, effects of microbiotic homogenization via invasive species pathways can be elucidated by modeling and monitoring relative to larger community and biome structure. Given that many invasive species are introduced through trade, Matt Gray discussed in his keynote address the importance of understanding pathogen movements in trade and factors that could influence spillover to wild populations (Gray et al. 2024).

Two observations were made when observing talks at the joint sessions of GARD24 and WCH10 that raised concerns. The first was that biosecurity practices were not very evident in presentations, for example glove use was minimal in photographs and hygiene practices were rarely discussed in procedures (e.g., acknowledgment of between-animal or between-site disinfection: e.g., Olson et al. 2021; Bletz et al. 2023). Publication of biosecurity 'best practices', such as in Gray et al. (2017), and reporting procedures in presentations could help elevate awareness of these issues across the herpetofaunal community. For example, Gray et al. (2018) demonstrated that not changing gloves between handling different amphibians can increase *Rv* transmission from infected to uninfected individuals by > 60%. If changing gloves is cost-prohibitive, latex or nitrile gloves can be disinfected then rinsed with clean water between animals (Gray et al. 2017). Disinfection of gear may similarly be cost- or time-prohibitive during field work, and practical measures might be considered such as the spatial scale of biosecurity applications (e.g., disinfection between watersheds rather than local wetland sites) and whether disease-causing pathogens are known to be emerging in an area or whether they are considered endemic. In this vein, we heard no mention of general biosecurity measures being endorsed or employed by 1500 meeting delegates who convened from all continents, many of whom brought their personal field gear and engaged in excursions to natural areas on Borneo. In herpetofaunal research studies and as those scientists travel with their field gear, herpetofaunal disease biosecurity measures are relevant considerations. In particular, best practices for large conferences warrant development and communication to delegates.

The second concern was a growing need to safeguard species locality information to prevent habitat overuse or species overcollection. This concern spans all topics at herpetological conferences where specific locality information may be revealed, including disease presentations, where the community may not be aware of, or considering such concerns. The herpetofaunal community might consider developing "best practices" on the spatial resolution of animal location data in presentations, publications, and publicly available databases, especially for vulnerable or at-risk species.

Michelle Christman of the US Fish and Wildlife Service and Partners in Amphibian and Reptile Conservation helped to lead a workshop on unsustainable and illegal trade at WCH10 and reported additional cross-disciplinary concerns around trade and disease transmission. Challenges discussed related to the associated disease risks of confiscated reptiles and amphibians in the illegal trade, and related barriers that affect returning confiscated animals to their native home-range. For example, several cases exist of seized amphibians either being infected with amphibian chytrid fungi or being prohibited for importation due to being listed as injurious due to chytrid susceptibility (e.g., Zevallos et al. 2016, U.S. Attorney's Office 2024). This situation is known to occur among other herpetofauna hosts and pathogens (Bezerra-Santos et al. 2021) but has not been well monitored or published (Gómez and Aguirre 2008). Disease risk also limits the ability of zoos and wildlife rehabilitation centers to accept confiscated animals owing to the cost of quarantine and testing. This is further aggravated as many animals in the illegal trade are more susceptible to infection because they are often housed with mixed species and undergo stressful shipping practices (e.g., turtles often experience intentional dehydration and are bound in duct tape and socks).

Similar disease-transmission challenges are being faced in legal trade markets. Dr. Rachel Marschang contributed an impromptu talk to fill a gap in a session (therefore, no abstract available) addressing *Ferlavirus* (also known as Ophidian paramyxovirus, a cause of respiratory and neurological diseases) in Northern Caiman Lizards (*Dracaena guianensis*; native to northern South America) that were in France and were being transported to Peru. This pathogen is more commonly reported in snakes, although turtles and lizards are known hosts, yet it is not tested for or managed in traded species. Matt Gray discussed how chytrid fungi and *Rv* cost businesses an estimated 140 million US dollars in annual revenue losses (Cavasos et al. 2023a). U.S. pet owners are willing to pay up to 75% more for amphibians that are certified as free from *Bd*, *Bsal* and *Rv* infection (Cavasos et al. 2023b). The Healthy Amphibian Trade Team (2024) began work with 20 stakeholders from industry, academia, and the government to develop "a voluntary program that would certify U.S. businesses as healthy trade partners" with a series of actions, including: 1) participation in online training; 2) incorporation of biosecurity practices to promote healthy animals; 3) testing a subset of resident, for-sale, and newly acquired amphibians for chytrid fungi and *Rv*; and 4) quarantining animals if a positive detection occurs. These efforts recently led to the creation of the Healthy Trade Institute, Inc. (2024), which is a non-profit organization that is empowering businesses to incorporate healthy trade practices into operations. Fostering proactive healthy-herpetofaunal practices in research, education and outreach, recreation, and trade is a challenging multi-sector endeavor, requiring integration of research scientists from biological and social science disciplines, wildlife managers, and broad stakeholder communities across geographiec scales (e.g., Olson and Pilliod 2022).

To build upon the existing momentum and enhanced communications and collaborations within amphibian and reptile disease research and conservation communities, a third reconvening of the GARD Conference is being planned for 8–12 June 2026 in Knoxville, Tennessee, USA (GARD26; more information will be released soon). It is hoped that some of the ‘future directions’ outlined above will have been developed further by this next convening of the global community.

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